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## RAW SEQUENCE LISTING

DATE: 01/12/2004

PATENT APPLICATION: US/10/650,369A

TIME: 10:36:11

Input Set : N:\CrF3\RULE60\10650369A.RAW.txt

Output Set: N:\CRF4\01092004\J650369A.raw

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1 <110> APPLICANT: Potter, Andrew A.
2   Perez-Casal, Jose
3   Fontaine, Michael
4 <120> TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
5   AGAINST STREPTOCOCCUS INFECTION
6 <130> FILE REFERENCE: 9000-0057
7 <140> CURRENT APPLICATION NUMBER: 10/650,369A
8 <141> CURRENT FILING DATE: 2003-08-27
9 <150> PRIOR APPLICATION NUMBER: US/09/878,766A
10 <151> PRIOR FILING DATE: 2001-09-10
11 <160> NUMBER OF SEQ ID NOS: 22
12 <170> SOFTWARE: PatentIn Ver. 2.0
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 37
16 <212> TYPE: DNA
17 <213> ORGANISM: Artificial Sequence
18 <220> FEATURE:
19 <223> OTHER INFORMATION: Description of Artificial Sequence: primer gapC1
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21   ggcggcggca tatggtagtt aaagttggta ttaacgg                                     37
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24 <211> LENGTH: 35
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Description of Artificial Sequence: primer gapClr
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30   gcggatcctt atttagcgat ttttgcaaag tactc                                     35
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33 <211> LENGTH: 32
34 <212> TYPE: DNA
35 <213> ORGANISM: Artificial Sequence
36 <220> FEATURE:
37 <223> OTHER INFORMATION: Description of Artificial Sequence: primer gap-1
38 <400> SEQUENCE: 3
39   aaaaaaggat ccggtatggt agttaaagtt gg                                       32
41 <210> SEQ ID NO: 4
42 <211> LENGTH: 39
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial Sequence
45 <220> FEATURE:
46 <223> OTHER INFORMATION: Description of Artificial Sequence: primer Gap-2
47 <400> SEQUENCE: 4

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48      aaaaaaacat ggttactcga gtgcttccag aacgatttc      39
50 <210> SEQ ID NO: 5
51 <211> LENGTH: 31
52 <212> TYPE: DNA
53 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <223> OTHER INFORMATION: Description of Artificial Sequence: primer Gap-3
56 <400> SEQUENCE: 5
57      aaaaaactcg aggtactgt agaagttaa g      31
59 <210> SEQ ID NO: 6
60 <211> LENGTH: 45
61 <212> TYPE: DNA
62 <213> ORGANISM: Artificial Sequence
63 <220> FEATURE:
64 <223> OTHER INFORMATION: Description of Artificial Sequence: primer Gap-4
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66      aaaaaaacat ggtaatcga tttcaagaac gatttcaaca ccgtc      45
68 <210> SEQ ID NO: 7
69 <211> LENGTH: 34
70 <212> TYPE: DNA
71 <213> ORGANISM: Artificial Sequence
72 <220> FEATURE:
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87 <211> LENGTH: 35
88 <212> TYPE: DNA
89 <213> ORGANISM: Artificial Sequence
90 <220> FEATURE:
91 <223> OTHER INFORMATION: Description of Artificial Sequence: primer Gap-7
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95 <210> SEQ ID NO: 10
96 <211> LENGTH: 42
97 <212> TYPE: DNA
98 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Description of Artificial Sequence: primer Gap-8
101 <400> SEQUENCE: 10
102      aaaaaaacat ggctattatt tagcgatttt tgcaaaatac tc      42

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104 <210> SEQ ID NO: 11
105 <211> LENGTH: 1011
106 <212> TYPE: DNA
107 <213> ORGANISM: Streptococcus dysgalactiae
108 <220> FEATURE:
109 <221> NAME/KEY: CDS
110 <222> LOCATION: (1)..(1011)
111 <400> SEQUENCE: 11
112      atg gta gtt aaa gtt ggt att aac ggt ttc ggt cgt atc gga cgt ctt      48
113      Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
114      1          5          10          15
115      gca ttc cgt cgt att caa aat gtt gaa ggt gtt gaa gta act cgt atc      96
116      Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
117      20          25          30
118      aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tac gat      144
119      Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
120      35          40          45
121      aca act caa gga cgt ttt gac gga act gtt gaa gtt aaa gaa ggt gga      192
122      Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly
123      50          55          60
124      ttt gaa gta aac gga aac ttc atc aaa gtt tct gct gaa cgt gat cca      240
125      Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro
126      65          70          75          80
127      gaa aac atc gac tgg gca act gac ggt gtt gaa atc gtt ctg gaa gca      288
128      Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
129      85          90          95
130      act ggt ttc ttt gct aaa aaa gaa gct gct gaa aaa cac tta cat gct      336
131      Thr Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu His Ala
132      100          105          110
133      aac ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga aac gac gtt      384
134      Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
135      115          120          125
136      aaa aca gtt gtt ttc aac act aac cac gac att ctt gac ggt act gaa      432
137      Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
138      130          135          140
139      aca gtt atc tca ggt gct tca tgt act aca aac tgt tta gct cct atg      480
140      Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
141      145          150          155          160
142      gct aaa gct ctt cac gat gca ttt ggt atc caa aaa ggt ctt atg act      528
143      Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr
144      165          170          175
145      aca atc cac gct tat act ggt gac caa atg atc ctt gac gga cca cac      576
146      Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
147      180          185          190
148      cgt ggt ggt gac ctt cgt cgt gct cgt gct ggt gct gca aac att gtt      624
149      Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val
150      195          200          205
151      cct aac tca act ggt gct gct aaa gct atc ggt ctt gtt atc cca gaa      672
152      Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu

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Input Set : N:\Crif3\RULE60\10650369A.RAW.txt

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153          210          215          220
154      ttg aat ggt aaa ctt gat ggt gct gca caa cgt gtt cct gtt cca act 720
155      Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
156      225          230          235          240
157      gga tca gta act gag ttg gtt gta act ctt gat aaa aac gtt tct gtt 768
158      Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val
159          245          250          255
160      gac gaa atc aac gct gct atg aaa gct gct tca aac gac agt ttc ggt 816
161      Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly
162          260          265          270
163      tac act gaa gat cca att gtt tct tca gat atc gta ggc gtg tca tac 864
164      Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Val Ser Tyr
165          275          280          285
166      ggt tca ttg ttt gac gca act caa act aaa gtt atg gaa gtt gac gga 912
167      Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Met Glu Val Asp Gly
168          290          295          300
169      tca caa ttg gtt aaa gtt gta tca tgg tat gac aat gaa atg tct tac 960
170      Ser Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
171      305          310          315          320
172      act gct caa ctt gtt cgt aca ctt gag tac ttt gca aaa atc gct aaa 1008
173      Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
174          325          330          335
175      taa 1011
177 <210> SEQ ID NO: 12
178 <211> LENGTH: 336
179 <212> TYPE: PRT
180 <213> ORGANISM: Streptococcus dysgalactiae
181 <400> SEQUENCE: 12
182      Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
183          1          5          10          15
184      Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
185          20          25          30
186      Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
187          35          40          45
188      Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly
189          50          55          60
190      Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro
191          65          70          75          80
192      Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
193          85          90          95
194      Thr Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu His Ala
195          100          105          110
196      Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
197          115          120          125
198      Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
199          130          135          140
200      Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
201          145          150          155          160
202      Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr

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203          165          170          175
204 Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
205          180          185          190
206 Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val
207          195          200          205
208 Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
209          210          215          220
210 Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
211          225          230          235          240
212 Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val
213          245          250          255
214 Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly
215          260          265          270
216 Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Val Ser Tyr
217          275          280          285
218 Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Met Glu Val Asp Gly
219          290          295          300
220 Ser Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
221          305          310          315          320
222 Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
223          325          330          335
225 <210> SEQ ID NO: 13
226 <211> LENGTH: 1011
227 <212> TYPE: DNA
228 <213> ORGANISM: Streptococcus agalactiae
229 <220> FEATURE:
230 <221> NAME/KEY: CDS
231 <222> LOCATION: (1)..(1011)
232 <400> SEQUENCE: 13
233 atg gta gtt aaa gtt ggt att aac ggt ttc ggt cgt atc ggt cgt ctt 48
234 Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
235 1 5 10 15
236 gca ttc cgt cgc atc caa aac gta gaa ggt gtt gaa gtt act cgt atc 96
237 Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
238 20 25 30
239 aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tat gac 144
240 Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
241 35 40 45
242 aca act caa ggt cgt ttc gac ggt act gtt gaa gtt aaa gaa ggt gga 192
243 Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly
244 50 55 60
245 ttc gaa gtt aac ggt caa ttt gtt aaa gtt tct gct gaa cgc gaa cca 240
246 Phe Glu Val Asn Gly Gln Phe Val Lys Val Ser Ala Glu Arg Glu Pro
247 65 70 75 80
248 gca aac att gac tgg gct act gat ggc gta gaa atc gtt ctt gaa gca 288
249 Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
250 85 90 95
251 act ggt ttc ttt gca tca aaa gaa aaa gct gga caa cac atc cat gaa 336
252 Thr Gly Phe Phe Ala Ser Lys Glu Lys Ala Gly Gln His Ile His Glu

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/650,369A

DATE: 01/12/2004  
TIME: 10:36:12

Input Set : N:\Crf3\RULE60\10650369A.RAW.txt  
Output Set: N:\CRF4\01092004\J650369A.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/650,369A

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Input Set : N:\Crf3\RULE60\10650369A.RAW.txt

Output Set: N:\CRF4\01092004\J650369A.raw

L:716 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:718 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21